

SEQUENCE LISTING

<110> Bermudes, G.  
King, I.  
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<120> COMPOSITIONS AND METHODS FOR  
TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES

<130> 8002-059

<150> 60/157,581  
<151> 1999-10-04

<150> 60/157,637  
<151> 1999-10-04

<160> 61

<170> FastSEQ for Windows Version 3.0

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<220>

<223> Forward primer

<400> 1  
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26

<210> 2  
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<220>

<223> Reverse primer

<400> 2  
cgggatccga gctcgagggc ccgggaaagg atctaagaag atcc

44

<210> 3  
<211> 477  
<212> DNA  
<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(474)

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Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His  
5 10 15

48

gta gtt gct aac cct cag gca gaa ggt cag ctg cag tgg ctg aac cgt Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg 20 25 30	96
cgc gct aac gcc ctg ctg gca aac ggc gtt gag ctc cgt gat aac cag Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln 35 40 45	144
ctc gtg gta cct tct gaa ggt ctg tac ctg atc tat tct caa gta ctg Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu 50 55 60	192
ttc aag ggt cag ggc tgc ccg tcg act cat gtt ctg ctg act cac acc Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr 65 70 75 80	240
atc agc cgt att gct gta tct tac cag acc aaa gtt aac ctg ctg agc Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser 85 90 95	288
gct atc aag tct ccg tgc cag cgt gaa act ccc gag ggt gca gaa gcg Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala 100 105 110	336
aaa cca tgg tat gaa ccg atc tac ctg ggt ggc gta ttt caa ctg gag Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Val Phe Gln Leu Glu 115 120 125	384
aaa ggt gac cgt ctg tcc gca gaa atc aac cgt cct gac tat cta gat Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp 130 135 140	432
ttc gct gaa tct ggc cag gtg tac ttc ggt att atc gca ctg Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu 145 150 155	474
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<210> 4	
<211> 158	
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Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His 1 5 10 15	
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg 20 25 30	
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln 35 40 45	
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu 50 55 60	
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr 65 70 75 80	
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser 85 90 95	
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala 100 105 110	
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Val Phe Gln Leu Glu 115 120 125	
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp 130 135 140	

Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu  
 145 150 155

<210> 5  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Forward primer

<400> 5 28  
 ccgacgcgtt gacacacctgaa aactggag

<210> 6  
 <211> 29  
 <212> DNA  
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<220>  
 <223> Reverse primer

<400> 6 29  
 ccgacgcgtg aaaggatctc aagaagatc

<210> 7  
 <211> 543  
 <212> DNA  
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<220>  
 <223> Fusion construct

<221> CDS  
 <222> (1)...(540)

<400> 7 48  
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 Met Lys Lys Thr Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
 1 5 10 15

acc gta gcg cag gcc cat atg gta cgt agc tcc tct cgc act ccg tcc 96  
 Thr Val Ala Gln Ala His Met Val Arg Ser Ser Arg Thr Pro Ser  
 20 25 30

gat aag ccg gtt gct cat gta gtt gct aac cct cag gca gaa ggt cag 144  
 Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln  
 35 40 45

ctg cag tgg ctg aac cgt cgc gct aac gcc ctg ctg gca aac ggc gtt 192  
 Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val  
 50 55 60

gag ctc cgt gat aac cag ctc gtg gta cct tct gaa ggt ctg tac ctg 240  
 Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu  
 65 70 75 80

atc tat tct caa gta ctg ttc aag ggt cag ggc tgc ccg tcg act cat 288  
 Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His  
 85 90 95

gtt ctg ctg act cac acc atc agc cgt att gct gta tct tac cag acc	336
Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr	
100 105 110	
aaa gtt aac ctg ctg agc gct atc aag tct ccg tgc cag cgt gaa act	384
Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr	
115 120 125	
ccc gag ggt gca gaa gcg aaa cca tgg tat gaa ccg atc tac ctg ggt	432
Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly	
130 135 140	
ggc gta ttt caa ctg gag aaa ggt gac cgt ctg tcc gca gaa atc aac	480
Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn	
145 150 155 160	
cgt cct gac tat cta gat ttc gct gaa tct ggc cag gtg tac ttc ggt	528
Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly	
165 170 175	
att atc gca ctg taa	543
Ile Ile Ala Leu	
180	

<210> 8  
 <211> 180  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Fusion construct

<400> 8	
Met Lys Lys Thr Ala Ile Ala Ile Val Ala Leu Ala Gly Phe Ala	
1 5 10 15	
Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser	
20 25 30	
Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln	
35 40 45	
Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val	
50 55 60	
Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu	
65 70 75 80	
Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His	
85 90 95	
Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr	
100 105 110	
Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr	
115 120 125	
Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly	
130 135 140	
Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn	
145 150 155 160	
Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly	
165 170 175	
Ile Ile Ala Leu	
180	

<210> 9  
 <211> 801  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Fusion construct

<221> CDS

<222> (1)...(798)

<400> 9		48
atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct		
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala		
1 5 10 15		
acc gta gcg cag gcc cat atg gct aac gag ctg aag cag atg cag gac		96
Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp		
20 25 30		
aag tac tcc aaa agt ggc att gct tgt ttc tta aaa gaa gat gac agt		144
Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser		
35 40 45		
tat tgg gac ccc aat gac gaa gag agt atg aac agc ccc tgc tgg caa		192
Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln		
50 55 60		
gtc aag tgg caa ctc cgt cag ctc gtt aga aag atg att ttg aga acc		240
Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr		
65 70 75 80		
tct gag gaa acc att tct aca gtt caa gaa aag caa aat att tct		288
Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser		
85 90 95		
ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct cac ata act		336
Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr		
100 105 110		
ggg acc aga gga aga agc aac aca ttg tct tct cca aac tcc aag aat		384
Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn		
115 120 125		
gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca tca agg agt		432
Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser		
130 135 140		
ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt gaa ctg gtc		480
Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val		
145 150 155 160		
atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca tac ttt cga		528
Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg		
165 170 175		
ttt cag gag gaa ata aaa gaa aac aca aag aac gac aaa caa atg gtc		576
Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val		
180 185 190		
caa tat att tac aaa tac aca agt tat cct gac cct ata ttg ttg atg		624
Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met		
195 200 205		

aaa agt gct aga aat agt tgg tct aaa gat gca gaa tat gga ctc	672
Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu	
210 215 220	
tat tcc atc tat caa ggg gga ata ttt gag ctt aag gaa aat gac aga	720
Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg	
225 230 235 240	
att ttt gtt tct gta aca aat gag cac ttg ata gac atg gac cat gaa	768
Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu	
245 250 255	
gcc agt ttt ttc ggg gcc ttt tta gtt ggc taa	801
Ala Ser Phe Phe Gly Ala Phe Leu Val Gly	
260 265	

<210> 10  
 <211> 266  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Fusion construct

<400> 10  
 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
 1 5 10 15  
 Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp  
 20 25 30  
 Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser  
 35 40 45  
 Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln  
 50 55 60  
 Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr  
 65 70 75 80  
 Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser  
 85 90 95  
 Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr  
 100 105 110  
 Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn  
 115 120 125  
 Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser  
 130 135 140  
 Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val  
 145 150 155 160  
 Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg  
 165 170 175  
 Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val  
 180 185 190  
 Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met  
 195 200 205  
 Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu  
 210 215 220  
 Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg  
 225 230 235 240  
 Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu  
 245 250 255  
 Ala Ser Phe Phe Gly Ala Phe Leu Val Gly  
 260 265

<210> 11  
<211> 465  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fusion construct

<221> CDS  
<222> (1) .... (462)

<400> 11 48  
atg aaa aag acg gct ctg gcg ctt ctg ctc ttg ctg tta gcg ctg act  
Met Lys Lys Thr Ala Leu Ala Leu Leu Leu Leu Leu Ala Leu Thr  
1 5 10 15  
agt gta gcg cag gcc gct cct act agc tcg agc act aag aaa act caa 96  
Ser Val Ala Gln Ala Ala Pro Thr Ser Ser Thr Lys Lys Thr Gln  
20 25 30  
ctg caa ttg gag cat ctg ctg gat ctg cag atg att ctg aat ggc 144  
Leu Gln Leu Glu His Leu Leu Asp Leu Gln Met Ile Leu Asn Gly  
35 40 45  
atc aat aac tac aag aac cct aag ctg act cgc atg ctg act ttc aaa 192  
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys  
50 55 60  
ttc tac atg ccg aaa aag gct acc gag ctc aaa cat ctc cag tgc ctg 240  
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu  
65 70 75 80  
gaa gag gaa ctg aag ccg ctg gag gaa gta ctt aac ctg gca cag tct 288  
Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser  
85 90 95  
aag aac ttc cac ctg cgt ccg cgt gac ctg atc tcc aac atc aat gta 336  
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val  
100 105 110  
atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac 384  
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr  
115 120 125  
gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc 432  
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr  
130 135 140  
ttt gcc caa tcg atc att agc acg tta act taa 465  
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr  
145 150

<210> 12  
<211> 154  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion construct

<400> 12  
 Met Lys Lys Thr Ala Leu Ala Leu Leu Leu Leu Leu Ala Leu Thr  
 1 5 10 15  
 Ser Val Ala Gln Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln  
 20 25 30  
 Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly  
 35 40 45  
 Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys  
 50 55 60  
 Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu  
 65 70 75 80  
 Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser  
 85 90 95  
 Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val  
 100 105 110  
 Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr  
 115 120 125  
 Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr  
 130 135 140  
 Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr  
 145 150

<210> 13  
 <211> 465  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Fusion construct

<221> CDS  
 <222> (1)...(462)

<400> 13  
 atg aaa cag tcg act ctg gcg ctt ctg ctc ttg ctg tta gcg ctg act 48  
 Met Lys Gln Ser Thr Leu Ala Leu Leu Leu Leu Ala Leu Thr  
 1 5 10 15  
 agt gtg gcc aaa gcg gct cct act agc tcg agc act aag aaa act caa 96  
 Ser Val Ala Lys Ala Ala Pro Thr Ser Ser Thr Lys Lys Thr Gln  
 20 25 30  
 ctg caa ttg gag cat ctg ctg gat ctg cag atg att ctg aat ggc 144  
 Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly  
 35 40 45  
 atc aat aac tac aag aac cct aag ctg act cgc atg ctg act ttc aaa 192  
 Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys  
 50 55 60  
 ttc tac atg ccg aaa aag gct acc gag ctc aaa cat ctc cag tgc ctg 240  
 Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu  
 65 70 75 80  
 gaa gag gaa ctg aag ccg ctg gag gaa gta ctt aac ctg gca cag tct 288  
 Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser  
 85 90 95  
 aag aac ttc cac ctg cgt ccg cgt gac ctg atc tcc aac atc aat gta 336  
 Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val  
 100 105 110

atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac 384  
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr  
115 120 125

gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc 432  
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr  
130 135 140

ttt gcc caa tcg atc att agc acg tta act taa 465  
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr  
145 150

<210> 14  
<211> 154  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion construct

<400> 14  
Met Lys Gln Ser Thr Leu Ala Leu Leu Leu Leu Leu Ala Leu Thr 15  
1 5 10 15  
Ser Val Ala Lys Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln 30  
20 25 30  
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly 45  
35 40 45  
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys 60  
50 55 60  
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu 80  
65 70 75 80  
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser 95  
85 90 95  
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val 110  
100 105 110  
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr 125  
115 120 125  
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr 140  
130 135 140  
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr  
145 150

<210> 15  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Forward primer

<400> 15 26  
agtctagaca atcaggcgaa gaacgg

<210> 16  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Reverse primer

<400> 16	25
agccatggag tcaccctcac ttttc	
<210> 17	
<211> 31	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Forward primer	
<400> 17	31
ggatccttaa gacccactt cacatttaag t	
<210> 18	
<211> 28	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Reverse primer	
<400> 18	28
gtttccatgg ttcactttc tctatcac	
<210> 19	
<211> 33	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Forward primer	
<400> 19	33
gtgtccatgg ggcacagcca ccgcgacttc cag	
<210> 20	
<211> 34	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Reverse primer	
<400> 20	34
acacgagctc ctacttggag gcagtcatga agct	
<210> 21	
<211> 72	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Forward primer	
<400> 21	60
gtgtccatgg ctcggggc aagtgtcggg actgaccatc atcatcatca tcacacagc	
caccgcact tc	72
<210> 22	
<211> 35	
<212> DNA	

<213> Artificial Sequence  
 <220>  
 <223> Reverse primer  
 <400> 22  
 gtgcggatcc ctacttggag gcagtcatga agctg 35

<210> 23  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 23  
 Met Ala Arg Arg Ala Ser Val Gly Thr Asp His His His His His  
 1 5 10 15

<210> 24  
 <211> 22  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide sequence TiP 13.40

<400> 24  
 Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg  
 1 5 10 15

Val Val Met Tyr Glu Gly  
 20

<210> 25  
 <211> 66  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Nucleotide sequence encoding TiP13.40

<400> 25  
 gcgtaccgct ggcgcctgtc ccatcgcccg aaaaccggct ttatccgcgt ggtgtatgtac 60  
 gaaggc 66

<210> 26  
 <211> 101  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 26  
 gtgtactagt gtggcgcagg cggcgtaccg ctggcgcctg tcccatcgcc cgaaaaccgg 60  
 ctttatccgc gtgggtatgt acgaaggcta aggatccgcg c 101

<210> 27  
 <211> 101  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 27  
 gcgccgatcc ttagccttcg tacatcacca cgccgataaa gccggtttc gggcgatggg 60  
 acaggcgcca gcggtacgcc gcctgcgcc aactagtaca c 101

<210> 28  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 28  
 Met Ser Ser Ala Ala Gly Phe Cys Ala Ser Arg Pro Gly Leu Leu Phe  
 1 5 10 15  
 Leu Gly Leu Leu Leu Pro Leu Val Val Ala Phe Ala Ser Ala Glu  
 20 25 30  
 Ala Glu Glu Asp Gly Asp Leu Gln Cys Leu Cys Val Lys Thr Thr Ser  
 35 40 45  
 Gln Val Arg Pro Arg His Ile Thr Ser Leu Glu Val Ile Lys Ala Gly  
 50 55 60  
 Pro His Cys Pro Thr Ala Gln Leu Ile Ala Thr Leu Lys Asn Gly Arg  
 65 70 75 80  
 Lys Ile Cys Leu Asp Leu Gln Ala Pro Leu Tyr Lys Lys Ile Ile Lys  
 85 90 95  
 Lys Leu Leu Glu Ser  
 100

<210> 29  
 <211> 106  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 29  
 cttcactagt gtggcgagg cgaacggccg caaaatctgc ctggacctgc aggcgcgcgt 60  
 gtacaaaaaa atcatcaaaa aactgctgga aagctaagga tccgcg 106

<210> 30  
 <211> 106  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 30  
 cgccggatcct tagcttcca gcagttttt gatgatttt ttgtacagcg gcgcctgcag 60  
 gtccaggcag atttgcggc cgttcgccctg cgccacacata gtgaag 106

<210> 31  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<400> 31  
 Ile Tyr Ser Phe Asp Gly Arg Asp Ile Met Thr Asp Pro Ser Trp Pro  
 1 5 10 15  
 Gln Lys Val Ile Trp His Gly Ser Ser Pro His Gly Val Arg Leu Val  
 20 25 30  
 Asp Asn Tyr Cys Glu Ala Trp Arg Thr Ala Asp Thr Ala Val Thr Gly  
 35 40 45

Leu Ala Ser Pro Leu Ser Thr Gly Lys Ile Leu Asp Gln Lys Ala Tyr  
 50 55 60  
 Ser Cys Ala Asn Arg Leu Ile Val Leu Cys Ile Glu Asn Ser Phe Met  
 65 70 75 80  
 Thr Asp Ala Arg Lys  
 85

<210> 32  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 32  
 ggcttcacta gtgtggcgca ggcgatatac tcctttgatg gtcg

44

<210> 33  
 <211> 37  
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 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

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37

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<400> 34

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<210> 36  
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<213> Artificial Sequence

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<220>
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<220>
<223> Reverse primer

<400> 46
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<210> 47
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<220>
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<400> 47
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<220>
<223> Reverse primer

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gaagataccc cgccggggccc gtccaccgtg tttcgcccgcc cg	
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98

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<400> 56

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100

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<210> 57  
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 <212> DNA  
 <213> Bacteriophage

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 <222> (7)...(408)

<221> modified\_base  
 <222> (1)...(1)  
 <223> n=a, c, g, or t

<400> 57

48

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Met Ala Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Met

1 5 10

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96

Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly Pro Ser Thr Val Phe Arg

15 20 25 30

ccg ccg acc tcc tcc cgc ccg ctg gaa acc ccg cat tgc cgc gaa atc

144

Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr Pro His Cys Arg Glu Ile

35 40 45

cgc atc ggc atc gcg ggc atc acc atc acc ctg tcc ctg tgc ggc tgc

192

Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser Leu Cys Gly Cys	50	55	60	
gcg aac gcg cgc gcg acc ctg cgc tcc gcg acc gcg gat aac tcc				240
Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr Ala Asp Asn Ser				
65	70	75		
gaa aac acc ggc ttt aaa aac gtc cgc gat ctg cgc acc gat cag ccg				288
Glu Asn Thr Gly Phe Lys Asn Val Pro Asp Leu Arg Thr Asp Gln Pro				
80	85	90		
aaa ccg ccg tcc aaa aaa cgc tcc tgc gat ccg tcc gaa tat cgc gtc				336
Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser Glu Tyr Arg Val				
95	100	105	110	
tcc gaa ctg aaa gaa tcc ctg atc acc acc acc ccg tcc cgc ccg				384
Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr Pro Ser Arg Pro Arg				
115	120	125		
acc gcc cgc cgc tgc atc cgc ctc tgaaagcttg gctgtttgg cggatgagag				438
Thr Ala Arg Arg Cys Ile Arg Leu				
130				
aagattttca gcctgataca gattaaatca gaacgcagaa gcggctctgat aaaacagaat				498
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<210> 58  
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 <212> PRT  
 <213> Bacteriophage

<400> 58				
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Thr Ser Ser Arg Pro Leu Glu Thr Pro His Cys Arg Glu Ile Arg Ile				
35	40	45		
Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser Leu Cys Gly Cys Ala Asn				
50	55	60		
Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr Ala Asp Asn Ser Glu Asn				
65	70	75	80	
Thr Gly Phe Lys Asn Val Pro Asp Leu Arg Thr Asp Gln Pro Lys Pro				
85	90	95		
Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser Glu Tyr Arg Val Ser Glu				
100	105	110		
Leu Lys Glu Ser Leu Ile Thr Thr Pro Ser Arg Pro Arg Thr Ala				
115	120	125		
Arg Arg Cys Ile Arg Leu				
130				

<210> 59  
 <211> 444  
 <212> DNA  
 <213> Bacteriophage

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 <222> (1)...(1)  
 <223> n=a, c, g, or t  
  
 <221> CDS

<222> (7)...(427)

<400> 59

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Arg Gln Arg Arg Arg Met Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly	
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ccg tcc acc gtg ttt cgc ccg acc tcc tcc cgc ccg ctg gaa acc	144
Pro Ser Thr Val Phe Arg Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr	
35 40 45	
ccg cat tgc cgc gaa atc cgc atc ggc atc gcg ggc atc acc atc acc	192
Pro His Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr	
50 55 60	
ctg tcc ctg tgc ggc tgc gcg aac gcg cgc gcg ccg acc ctg cgc tcc	240
Leu Ser Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser	
65 70 75	
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Ala Thr Ala Asp Asn Ser Glu Asn Thr Gly Phe Lys Asn Val Pro Asp	
80 85 90	
ctg cgc acc gat cag ccg aaa ccg ccg tcc aaa aaa cgc tcc tgc gat	336
Leu Arg Thr Asp Gln Pro Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp	
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